SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stern, David
Schmidt, Ann M.

(ii) TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED ATHEROSCLEROSIS USING (sRAGE) SOLUBLE RECEPTOR FOR ADVANCED GLYCATION ENDPRODUCTS

T0390X

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/905,709
(B) FILING DATE: 05-AUG-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/52876

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0526

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAAGGA TGGCAGCAGG GGCAGTGGTC GGAGCCTGGA TGCTAGTCCT CAGTCTGGGG 60

GGGACAGTCA CGGGGGACCA AAACATCACA GCCCGGATCG GGAAGCCACT GGTGCTGAAC 120

TGCAAGGGAG CCCCCAAGAA ACCACCCCAG CAGCTGGAAT GGAAACTGAA CACAGGCCGG 180

ACAGAAGCTT GGAAAGTCCT GTCTCCCCAG GGAGACCCCT GGGATAGCGT GGCTCGGGTC 240

CTCCCCAACG GCTCCCTCCT CCTGCCGGCT GTTGGGATCC AGGATGAGGG GACTTTCCGG 300

TGCCGGGCAA CGAGCCGGAG CGGAAAGGAG ACCAAGTCTA ACTACCGAGT CCGAGTCTAT 360

CAGATTCCTG GGAAGCCAGA AATTGTTGAT CCTGCCTCTG AACTCATGGC TGGTGTCCCC 420

AATAAGGTGG GGACATGTGT GTCCGAGGGG GGCTACCCTG CAGGGACTCT TAACTGGCTC 480

TTGGATGGGA AACTCTGATT CCTGATGGCA AAGGAGTGTC AGTGAAGGAA GAGACCAAGA 540

GACACCCAAA GACAGGGCTT TTCACTCTCC ATTCGGAGCT GATGGTGACC CCAGCTCGGG 600

GAGGAGCTCT CCACCCCACC TTCTCCTGTA GCTTCACCCC TGGCCTTCCC CGGCGCCGAG 660

CCCTGCACAC GGCCCCCATC CAGCTCAGGG TCTGGAGTGA GCACCGAGGT GGGGAGGGCC 720

CCAACGTGGA CGCTGTGCCA CTGAAGGAAG TCCAGTTGTG GTAGAGCCAG AAGGGGGAGC 780

AGTAGCTCCT GGTGGTACTG TGACCTTGAC CTGTGAAGCC CCCGCCCAGC CCCCACCTCA 840

AATCCACTGG ATCAAGGATG GCAGGCCCCT GCCCCTTCCC CCTGGCCCCA TGCTGCTCCT 900

CCCAGAGGTA GGGCCTGAGG ACCAGGGAAC CTACAGTTGT GTGGCCACCC ATCCCAGCCA 960

TGGGGGGGAG GAGAGCCGTG CTGTCAGCGT CACGATCATC GAAACAGGCG AGGAGGGGAC 1020

GACTGCAGGC TCTGTGGAAG GGCCGGGGCT GGAAACCTAG CCCTGACCCT GGGGATCCTG 1080

GGAGGCCTGG GGACAGTCGC CCTGCTCATT GGGGTCATCG TGTGGCATCG AAGGCCGGCA 1140

ACGCAAAGGA CAGGAGAGGA AGGTCCCGGA AAACCAGGAG GAGGAAGAGG AGGAGAGAGC 1200

GGAACTGAAC CAGCCAGAGG AGCCCGAGGC GGCAGAGAGC AGCACAGGAG GGCCTTGAGG 1260

AGCCCACGGC CAGACCCGAT CCATCAGCCC CTTTTCTTTT CCCACACTCT GTTCTGGCCC 1320

CAGACCAGTT CTCCTCTGTA TAATCTCCAG CCCACATCTC CCAAACTTTC TTCCACAACC 1380

AGAGCCTCCC ACAAAAAGTG ATGAGTAAAC ACCTGCCACA TTTAAAAAAA AAAAAAAA 1438

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGAGAGGTT GTAGCGATGT AGAGAGGTCA TGATGAAGGT CGGAGTGTGG TTGTTAGGAT 60

CTGATAGGGA GGAAGGTTTC AAGGGGTCAT GATTGGTTAG GGTATGGGGT AGGAAATGG 119

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGGCAGCCG GAACAGCAGT TGGAGCCTGG GTGCTGGTCC TCAGTCTGTG GGGGGCAGTA 60

GTAGGTGCTC AAAACATCAC AGCCCGGATT GGCGAGCCAC TGGTGCTGAA GTGTAAGGGG 120

GCCCCCAAGA AACCACCCCA GCGGCTGGAA TGGAAACTGA ACACAGGCCG GACAGAAGCT 180

TGGAAGGTCC TGTCTCCCCA GGGAGGAGGC CCCTGGGACA GTGTGGCTCG TGTCCTTCCC 240

AACGGCTCCC TCTTCCTTCC GGCTGTCGGG ATCCAGGATG AGGGGATTTT CCGGTGCAGG 300

GCAATGAACA GGAATGGAAA GGAGACCAAG TCCAACTACC GAGTCCGTGT CTACCAGATT 360

CCTGGGAAGC CAGAAATTGT AGATTCTGCC TCTGAACTCA CGGCTGGTGT TCCCAATAAG 420

GTGGGGACAT GTGTGTCAGA GGGAAGCTAC CCTGCAGGGA CTCTTAGCTG GCACTTGGAT 480

GGGAAGCCCC TGGTGCCTAA TGAGAAGGGA GTATCTGTGA AGGAACAGAC CAGGAGACAC 540

CCTGAGACAG GGCTCTTCAC ACTGCAGTCG GAGCTAATGG TGACCCCAGC CCGGGGAGGA 600

GATCCCCGTC CCACCTTCTC CTGTAGCTTC AGCCCAGGCC TTCCCCGACA CCGGGCCTTG 660

CGCACAGCCC CCATCCAGCC CCGTGTCTGG GAGCCTGTGC CTCTGGAGGA GGTCCAATTG 720

GGTGGTGGAG CCAGAAGGTG GAGCAGTAGC TCCTGGTGGA ACCGTAACCC TGACCTGTGA 780

AGTCCCTGCC CAGCCCTCTC CTCAAATCCA CTGGATGAAG GATGGTGTGC CCTGCCCCTT 840

CCCCCCAGCC CTGTGCTGAT CCTCCCTGAG ATAGGGCCTC AGGACCAGGG AACCTACAGC 900

TGTGTGGCCA CCCATTCCAG CCACGGGCCC CAGGAAAGCC GTGCTGTCAG CATCAGCATC 960

ATCGAACCAG GCGAGGAGGG GCCAACTGCA GGCTCTGTGG GAGGATCAGG GCTGGGAACT 1020

CTAGCCCTGG CCCTGGGGAT CCTGGGAGGC CTGGGGACAG CCGCCCTGCT CATTGGGGTC 1080

ATCTTGTGGC AAAGGCGGCA ACGCCGAGGA GAGGAGAGGA GGCCCCAGAA AACCAGGAGG 1140

AAGAGGAGGA GCGTGCAGAA CTGAATCAGT CGGAGGAACC TGAGGCAGGC GAGAGTACTA 1200

CTGGAGGGCC TTGAGGGGCC CACAGACAGA TCCCATCCAT CAGCTCCCTT TTCTTTTTCC 1260

CTTGAACTGT TCTGGCCTCA GACCAACTCT CTCCTGTATA ATCTCTCTCC TGTATAACCC 1320

CACCTTGCCA AGCTTTCTTC TACAACCAGA GCCCCCCACA ATGATGATTA AACACCTGAC 1380

ACATCTTTGC AAAAAAAAAA AAAAA 1405

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAGAGAGAG ATAGCGATGT AGGGAGAGGC AGTGATAGGT CGAGTGGTTG TTAGGTCGAT 60

AGGAAGGTTT CAGGGTCATG AGGTAGGGGG TAAGGGGTAA GGAAAGTGG 109